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<120> PLAG gene family and tumorigenesis

<130> VIB-011-US

<140> US 09/242,772
<141> 1999-06-25

<150> EP 96202229.6
<151> 1996-08-22

<150> EP 97200130.9
<151> 1997-01-17

<150> PCT/EP97/04759
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<210> 101
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<223> MV6 primer (PLAG 1 primer of second round RT-PCR)

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<210> 102
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<223> CTNNB1 primer of first round RT-PCR (CAT-UP)

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<210> 105
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<223> CTNNB1 primer of first round RT-PCR (CAT3)

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<210> 107

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<210> 108
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<213> Artificial Sequence

<220>
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1 5

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<213> Homo sapiens

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<400> 113

His Asp Leu Ser Glu Val Arg Asp Thr Gln Lys Val Pro Ser Gly Lys
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Arg

<210> 114
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His Phe Ser Ser Thr Ser Tyr Ala Ile Ser Ile Pro Glu Lys Glu Gln
1 5 10 15

Pro Leu

<210> 115
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<223> 8-Multiple Antigen Peptide

<400> 115

His Gln Leu Pro Thr Gln Thr Gln Asp Leu Gln Asp Pro
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ggccgtattt ggcacccaga atgcttcatt ctgtgacggt ctattaataa ggttgccttg 240

ctagagtttg gagcagggcc tcagattggc caaaatggga aggattggat tccactctct 300

tccacgaaga gtcaatggga ctggctaaga tcaaagtctg aggctttttc catcagtaat 360

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tcatttagtg gagttgggca gttcccaagt gtccaacaag aaggcctggt ttaggctgcg 480

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<211> 28
<212> PRT
<213> Homo sapiens

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Lys Val His Ser Tyr Ser His Thr Gly Glu Arg Pro
20 25

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Lys Leu Gln Arg His Met Ala Thr His Ser Pro Glu Lys Thr
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<210> 119
<211> 29
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<213> Homo sapiens

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His Lys Cys Asn Tyr Cys Glu Lys Met Phe His Arg Lys Asp His Leu
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Lys Asn His Leu His Thr His Asp Pro Asn Lys Glu Thr
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<223> PLAG 1 zinc finger 4

<400> 120

Phe Lys Cys Glu Glu Cys Gly Lys Asn Tyr Asn Thr Lys Leu Gly Phe
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Lys Arg His Leu Ala Leu His Ala Ala Thr Ser Gly Asp
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<211> 35
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<400> 121

Leu Thr Cys Lys Val Cys Leu Gln Thr Phe Glu Ser Thr Gly Val Leu
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Glu Lys Lys
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His Gln Cys Glu His Cys Asp Arg Arg Phe Tyr Thr Arg Lys Asp Val
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Arg Arg His Met Val Val His Thr Gly Arg Lys Asp
20 25

<210> 123
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1 5 10 15

Thr Arg His Met Lys Lys Ser His Asn Gln Glu Leu Leu
20 25

<210> 124
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<212> DNA
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Met
1

gct acc cat tct ccc cag aaa tct cac cag tgt gct cac tgt gag aag 227
Ala Thr His Ser Pro Gln Lys Ser His Gln Cys Ala His Cys Glu Lys
5 10 15

acg ttc aac cgg aaa gac cac ctg aaa aac cac ctc cag acc cac gac 275
Thr Phe Asn Arg Lys Asp His Leu Lys Asn His Leu Gln Thr His Asp
20 25 30

ccc aac aaa atg gcc ttt ggg tgt gag gag tgt ggg aag aag tac aac 323
Pro Asn Lys Met Ala Phe Gly Cys Glu Glu Cys Gly Lys Lys Tyr Asn
35 40 45

acc atg ctg ggc tat aag agg cac ctg gcc ctc cat gcg gcc agc agt 371
Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu His Ala Ala Ser Ser
50 55 60 65

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Gly Asp Leu Thr Cys Gly Val Cys Ala Leu Glu Leu Gly Ser Thr Glu
70 75 80

gtg cta ctg gac cac ctc aaa gcc cat gcg gaa gag aag ccc cct agc 467
Val Leu Leu Asp His Leu Lys Ala His Ala Glu Glu Lys Pro Pro Ser
85 90 95

gga acc aag gaa aag aag cac cag tgc gac cac tgt gaa aga tgc ttc 515
Gly Thr Lys Glu Lys Lys His Gln Cys Asp His Cys Glu Arg Cys Phe
100 105 110

tac acc cgg aag gat gtg cga cgc cac ctg gtg gtc cac aca gga tgc 563
Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val Val His Thr Gly Cys
115 120 125

aag gac ttc ctg tgc cag ttc tgt gcc cag aga ttt ggg cgc aag gtt 611
Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg Phe Gly Arg Lys Val
130 135 140 145

cac ctc acc cgg cat acc aag aag acc cac tca cag gag ctg atg aaa 659
His Leu Thr Arg His Thr Lys Lys Thr His Ser Gln Glu Leu Met Lys
150 155 160

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gag agc ttg cag acc gga gac ctt ctg agc acc ttc cac acc atc tcg      707
Glu Ser Leu Gln Thr Gly Asp Leu Leu Ser Thr Phe His Thr Ile Ser
            165                 170                 175

cct tca ttc caa ctg aag gct gct gcc ttg cct cct ttc cct tta gga      755
Pro Ser Phe Gln Leu Lys Ala Ala Ala Leu Pro Pro Phe Pro Leu Gly
        180                 185                 190

gct tct gcc cag aac ggg ctt gca agt agc ttg cca gct gag gtc cat      803
Ala Ser Ala Gln Asn Gly Leu Ala Ser Ser Leu Pro Ala Glu Val His
    195                 200                 205

agc ctc acc ctc agt ccc cca gaa caa gcc gcc cag cct atg cag ccg      851
Ser Leu Thr Leu Ser Pro Pro Glu Gln Ala Ala Gln Pro Met Gln Pro
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ctg cca gag tcc ctg gcc tcc ctc cac ccc tcg gta tcc cct ggc tct      899
Leu Pro Glu Ser Leu Ala Ser Leu His Pro Ser Val Ser Pro Gly Ser
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cct ccg cca ccc ctt ccc aat cac aag tac aac acc act tct acc tca      947
Pro Pro Pro Pro Leu Pro Asn His Lys Tyr Asn Thr Thr Ser Thr Ser
            245                 250                 255

tac tcc cca ctt gca agc ctg ccc ctc aaa gca gat act aaa ggt ttt      995
Tyr Ser Pro Leu Ala Ser Leu Pro Leu Lys Ala Asp Thr Lys Gly Phe
        260                 265                 270

tgc aat atc agt ttg ttt gag gac ttg cct ctg caa gag cct cag tca     1043
Cys Asn Ile Ser Leu Phe Glu Asp Leu Pro Leu Gln Glu Pro Gln Ser
    275                 280                 285

cct caa aag ctc aac cca ggt ttt gat ctg gct aag gga aat gct ggt     1091
Pro Gln Lys Leu Asn Pro Gly Phe Asp Leu Ala Lys Gly Asn Ala Gly
290                 295                 300                 305

aaa gta aac ctg ccc aag gag ctg cct gca gat gct gtg aac cta aca     1139
Lys Val Asn Leu Pro Lys Glu Leu Pro Ala Asp Ala Val Asn Leu Thr
                310                 315                 320

ata cct gcc tct ctg gac ctg tcc ccc ctg ttg ggc ttc tgg cag ctg     1187
Ile Pro Ala Ser Leu Asp Leu Ser Pro Leu Leu Gly Phe Trp Gln Leu
            325                 330                 335

ccc cct cct gct acc caa aat acc ttt ggg aat agc act ctt gcc ctg     1235
Pro Pro Pro Ala Thr Gln Asn Thr Phe Gly Asn Ser Thr Leu Ala Leu
        340                 345                 350

ggg cct ggg gaa tct ttg ccc cac agg tta agc tgt ctg ggg cag cag     1283
Gly Pro Gly Glu Ser Leu Pro His Arg Leu Ser Cys Leu Gly Gln Gln
    355                 360                 365

cag caa gaa ccc cca ctt gcc atg ggc act gtg agc ctg ggc cag ctc     1331
Gln Gln Glu Pro Pro Leu Ala Met Gly Thr Val Ser Leu Gly Gln Leu
370                 375                 380                 385

ccc ctg ccc ccc atc cct cat gtg ttc tca gct ggc act ggc tct gcc     1379
Pro Leu Pro Pro Ile Pro His Val Phe Ser Ala Gly Thr Gly Ser Ala
                390                 395                 400

atc ctg cct cat ttc cat cat gca ttc aga taa ttgattttta aagtgtattt   1432
Ile Leu Pro His Phe His His Ala Phe Arg
            405                 410
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ttccgtattc tggaagatgt tttaagaagc attttaaatg tcagttacaa tatgagaaag 1492

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<400> 125

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20 25 30

Asp Pro Asn Lys Met Ala Phe Gly Cys Glu Glu Cys Gly Lys Lys Tyr
35 40 45

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Asn Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu His Ala Ala Ser
    50                  55                  60

Ser Gly Asp Leu Thr Cys Gly Val Cys Ala Leu Glu Leu Gly Ser Thr
65                  70                  75                  80

Glu Val Leu Leu Asp His Leu Lys Ala His Ala Glu Glu Lys Pro Pro
                85                  90                  95

Ser Gly Thr Lys Glu Lys Lys His Gln Cys Asp His Cys Glu Arg Cys
            100                 105                 110

Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val Val His Thr Gly
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Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg Phe Gly Arg Lys
    130                 135                 140

Val His Leu Thr Arg His Thr Lys Lys Thr His Ser Gln Glu Leu Met
145                 150                 155                 160

Lys Glu Ser Leu Gln Thr Gly Asp Leu Leu Ser Thr Phe His Thr Ile
                165                 170                 175

Ser Pro Ser Phe Gln Leu Lys Ala Ala Leu Pro Pro Phe Pro Leu
            180                 185                 190

Gly Ala Ser Ala Gln Asn Gly Leu Ala Ser Ser Leu Pro Ala Glu Val
        195                 200                 205

His Ser Leu Thr Leu Ser Pro Pro Glu Gln Ala Ala Gln Pro Met Gln
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Pro Leu Pro Glu Ser Leu Ala Ser Leu His Pro Ser Val Ser Pro Gly
225                 230                 235                 240

Ser Pro Pro Pro Pro Leu Pro Asn His Lys Tyr Asn Thr Thr Ser Thr
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Ser Tyr Ser Pro Leu Ala Ser Leu Pro Leu Lys Ala Asp Thr Lys Gly
            260                 265                 270

Phe Cys Asn Ile Ser Leu Phe Glu Asp Leu Pro Leu Gln Glu Pro Gln
        275                 280                 285

Ser Pro Gln Lys Leu Asn Pro Gly Phe Asp Leu Ala Lys Gly Asn Ala
    290                 295                 300
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Gly Lys Val Asn Leu Pro Lys Glu Leu Pro Ala Asp Ala Val Asn Leu
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Thr Ile Pro Ala Ser Leu Asp Leu Ser Pro Leu Leu Gly Phe Trp Gln
325 330 335

Leu Pro Pro Pro Ala Thr Gln Asn Thr Phe Gly Asn Ser Thr Leu Ala
340 345 350

Leu Gly Pro Gly Glu Ser Leu Pro His Arg Leu Ser Cys Leu Gly Gln
355 360 365

Gln Gln Gln Glu Pro Pro Leu Ala Met Gly Thr Val Ser Leu Gly Gln
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Leu Pro Leu Pro Pro Ile Pro His Val Phe Ser Ala Gly Thr Gly Ser
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Ala Ile Leu Pro His Phe His His Ala Phe Arg
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gttggacatg gccatggaac cagacagaaa agcggctgtt agtcactggc agcaacagtc 300

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aggcaatcct gaggaagagg atgtggatac ctcccaagtc ctgtatgagt gggaacaggg 420

attttctcag tccttcactc aagaacaagt agctgatatt gatggacagt atgcaatgac 480

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cccatctaca cagtttgatg ctgctcatcc cactaatgtc cagcgtttgg ctgaaccatc 600

acagatgctg aaacatgcag ttgtaaactt gattaactat caagatgatg cagaacttgc 660

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aaaaaaaaga acaaaataaa atagcaaaac atttttaaga gtgtagattc tttgaaatta 120

aaggacatac ttaccctgta gt 142

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<211> 212
<212> DNA
<213> Homo sapiens

<220>
<221> STS
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<223> CH280

<400> 128
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acctttatat gtggttgaat tcttgttctt ggtttcacag aaggtatatt agcaaagcat 180

ttttggtgtt gaagcttggt ctgtgatcta gt 212

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<212> DNA
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gtaatagctg ggggttttct cacaagtcaa agacaaattg tctgttttca agcgtgtgaa 180

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tacag 245

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<223> EM156

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ggcaacttat aattattaac tgtggaatat ctttgaaaaa tgtttttngc agamgttatg 180

ttcccattcc tgactggmgc tcattataaa tacccatctt ctctgaatag cgcaaggact 240

tttgaaaaag tgttctgagt aaac 264

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tatcgcccng gcnvcagtgc agtggcacaa tctcaactca ctgcaacctc tgcctgccag 180

ggtcaagtga ttcttgtgcc tcagagtccc aagtacctgg gattacaggc ataagccacc 240

acgcctggct aaattttgta ttttcagtag tgacggggtt tcaccatgtt ggccaggctg 300

tctcaaactg ctgacctcag gtaatccacc ctcctcagcc tcccagagtt ctgggattac 360

aggcgtgaca ccgtgcctgg ctcattttat tttttagaga tgagatctca ctctkwttgc 420

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taattaaaga tatttttata aaavvtactc taggcccata aggcttcaca ggttaattgt 180

attaaatatt taaggaaaaa ataataccaa tcttattcat agtctttcag aaaatagagg 240

cgtatccatt tttctaactc attttaagaa atagcatcat tctaatatca aaagcaaaca 300

aggmcattgc aaagaagaag gggaagaagg aagaggaaga ggaggagaaa gggaagcagg 360

agatggagaa gaaggaagcc aggtacagtg caatatttct catgaacata aacacaattt 420

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gtacacaatg atgatgtcac acaattaatt acctattaag actgaaatcc agcaatgcat 180

agkgtgtgga ctttacgcac atccagaaaa agttctagca caaattgttt thgtmtyata 240

tatttcagaa gccatagaaa cactattaaa gccctcccta atcacttagg gatgcaaaat 300

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<212> DNA
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caaataattt ttaaagttta agccccttc tgacatgaca cgtccatggg tccttcaccc 180

ttyttkktct cctscagagc tccagtctgc cyyttyttks ctctgagctc caaaamcagt 240

gawtcccctg aagttaccta gmcccmccat acagtttgtg actccctawm ccgggggtac 300

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<212> DNA
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<222> (1)..(300)
<223> EM416

<220>
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tatwactcct gtgactggag ctgatggtgt cttaaggaaa gtggtgggaa gggaggvctg 180

cagaaaggca aggctggagt cgactgaagg ctggagagcc actgctttaa caagtgtamc 240

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<212> DNA
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actagagata taaggcttag gaaaaaagtg aatactacga taaatgaata ctaggaaaag 240

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aargaaa 307

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<212> DNA
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<220>
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<222> (1)..(164)
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acattgagga cttctggttg aaaattacag agtggtgaag attc 164